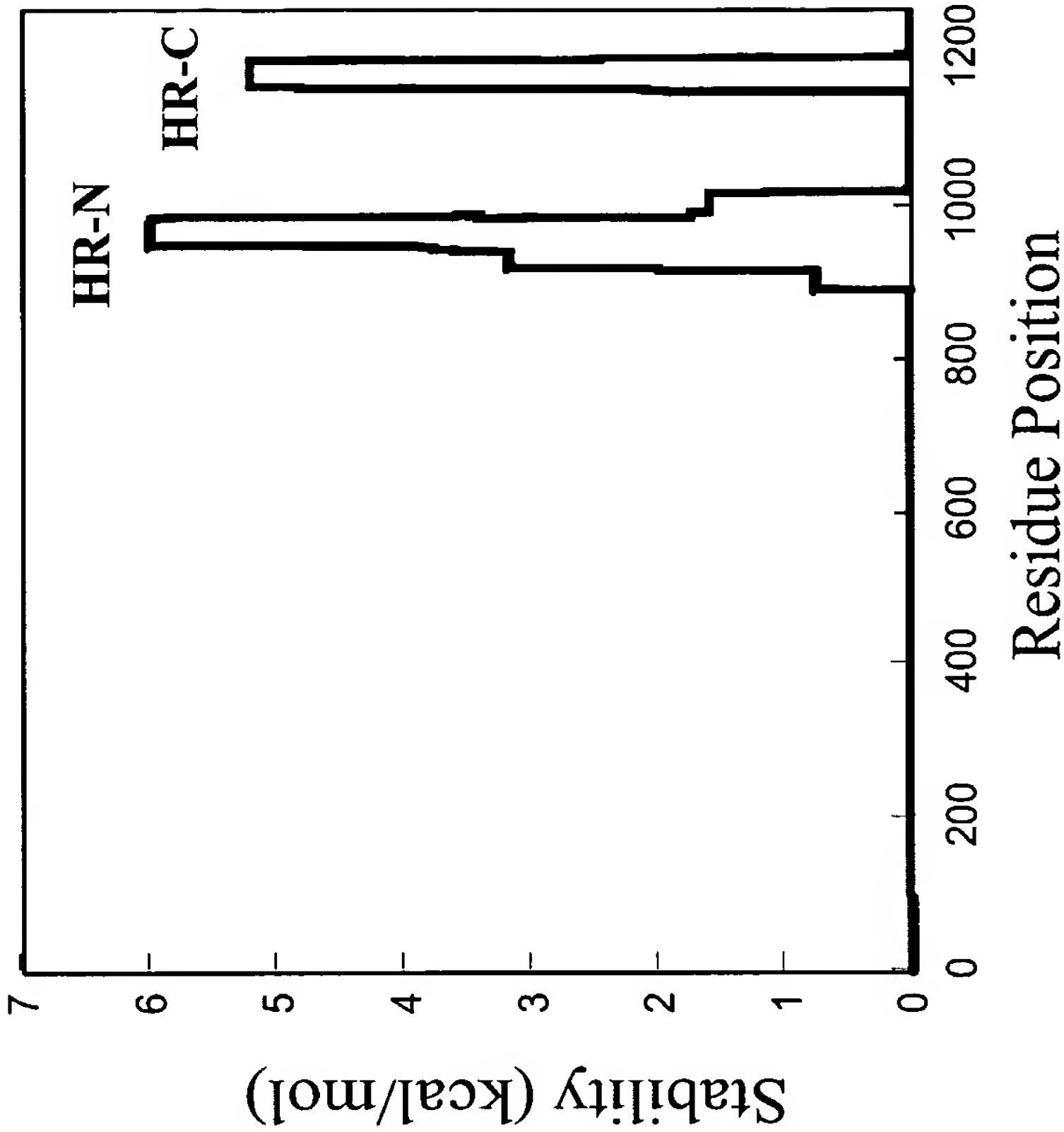


A



B

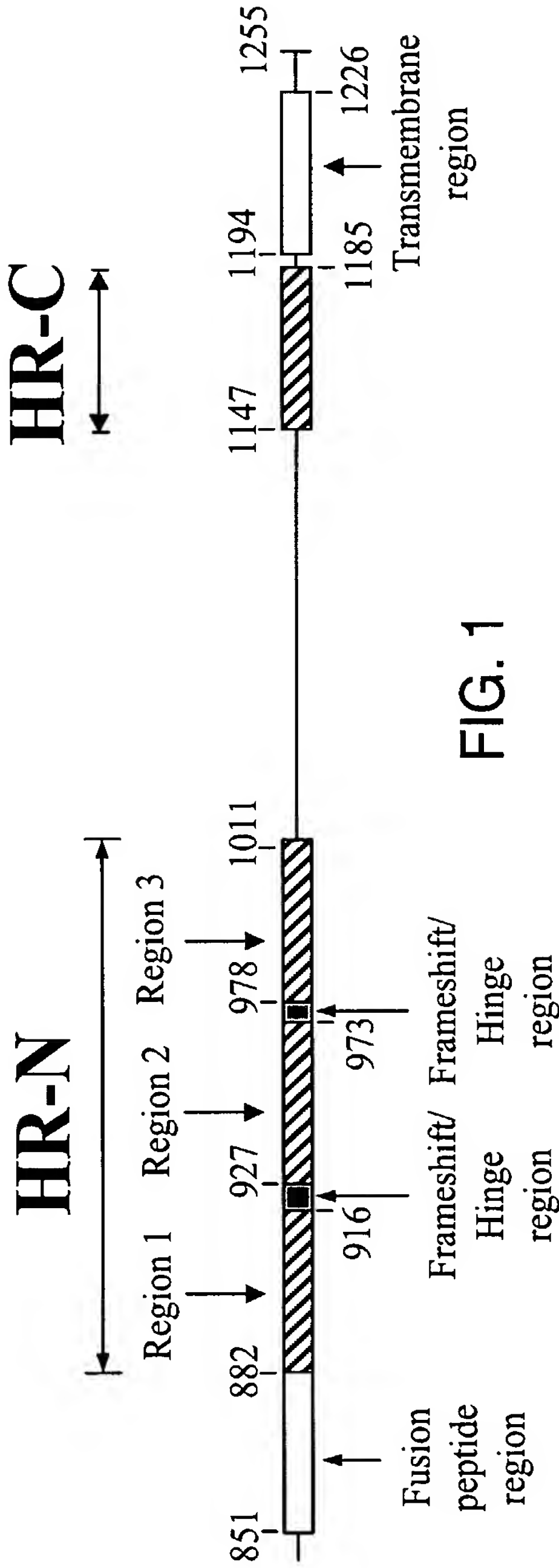
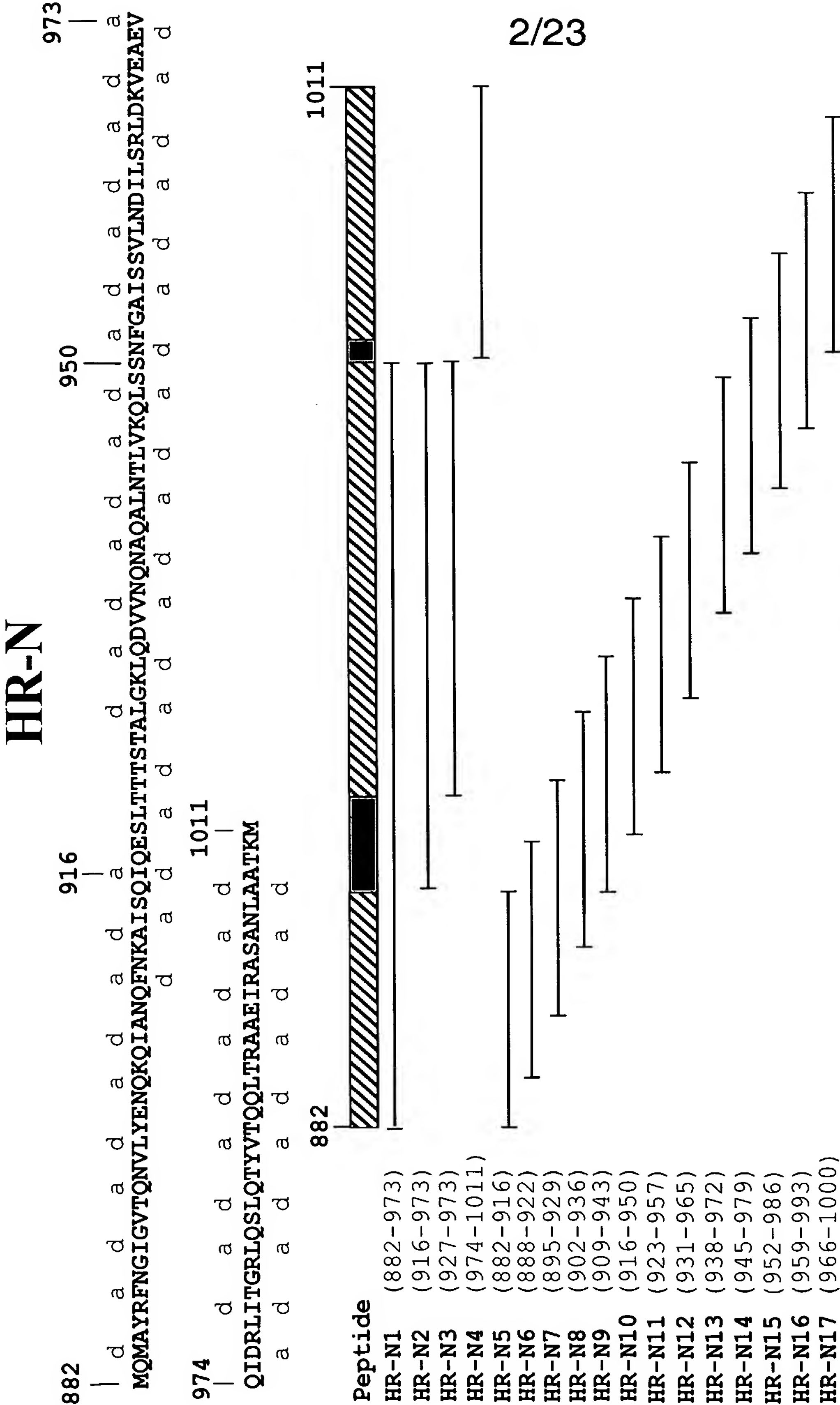


FIG. 1



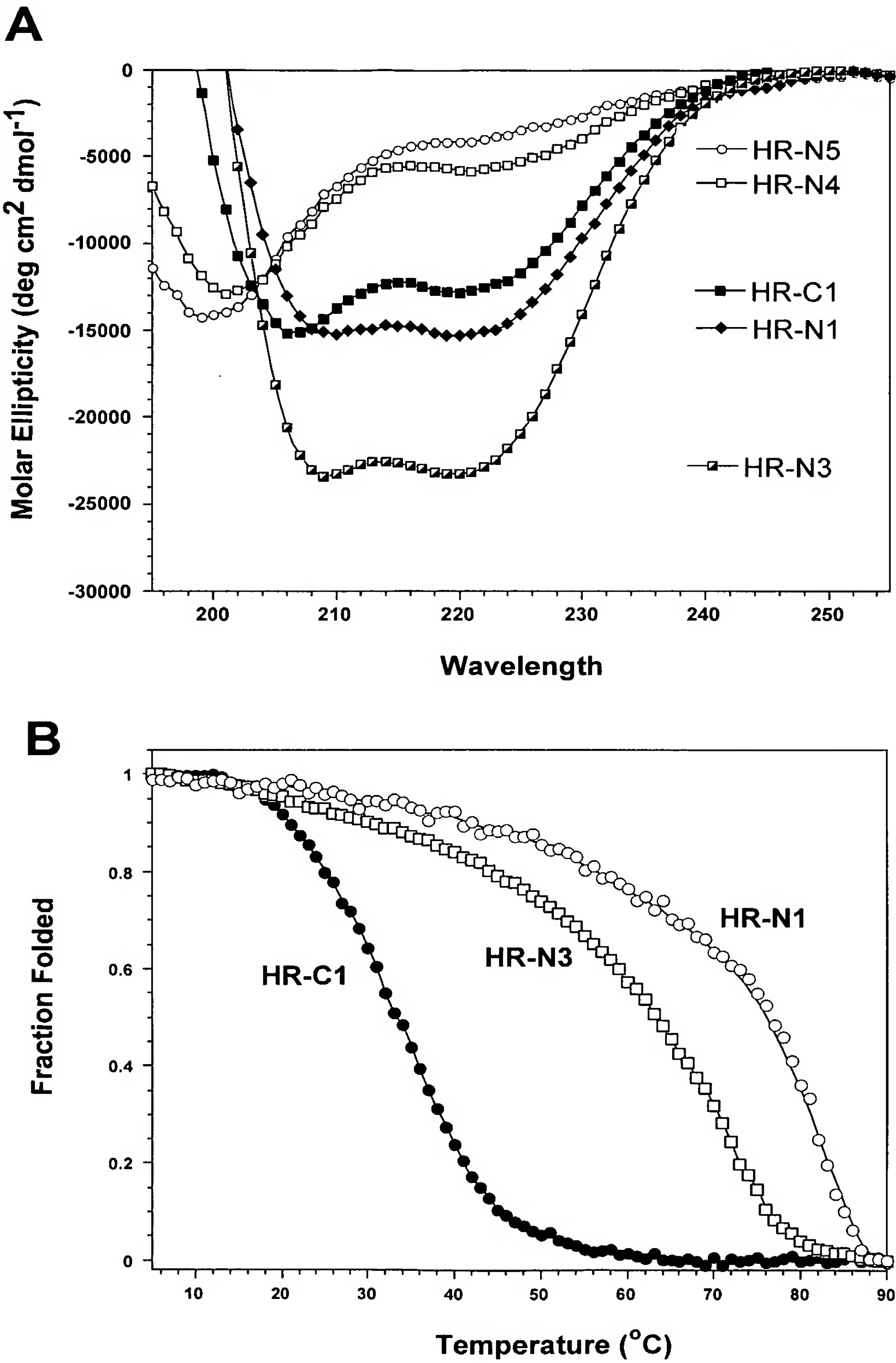


FIG. 3

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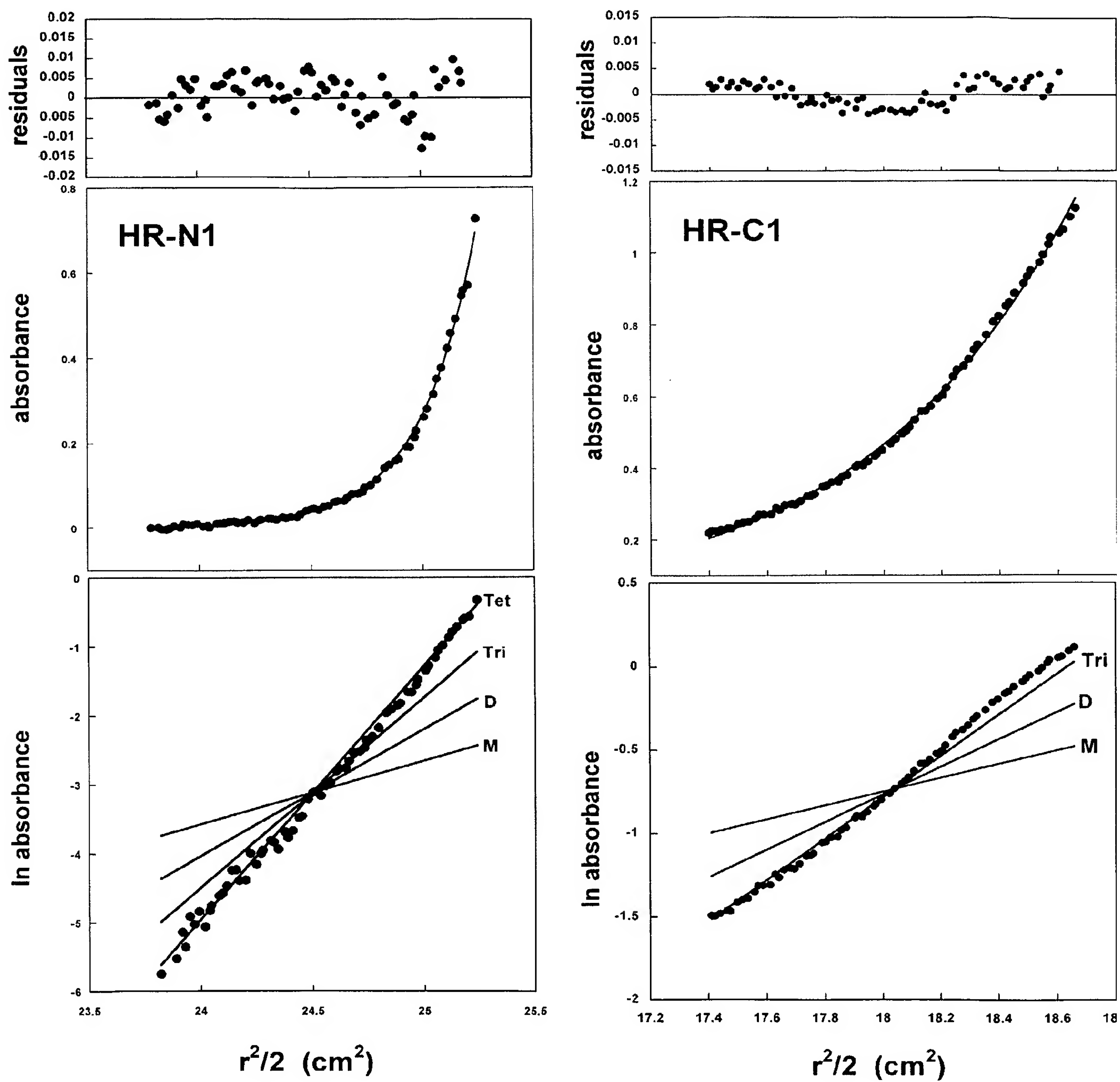


FIG. 4

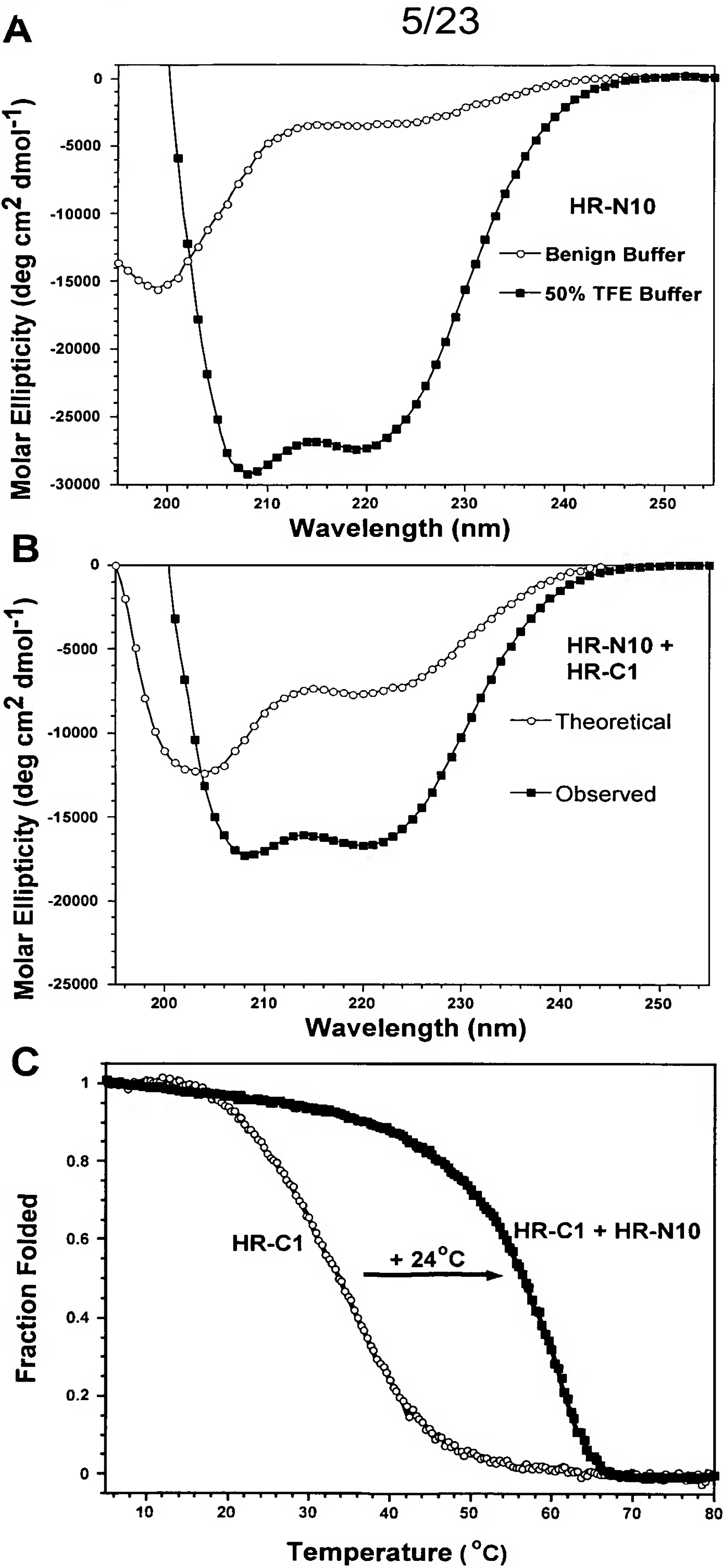


FIG. 5

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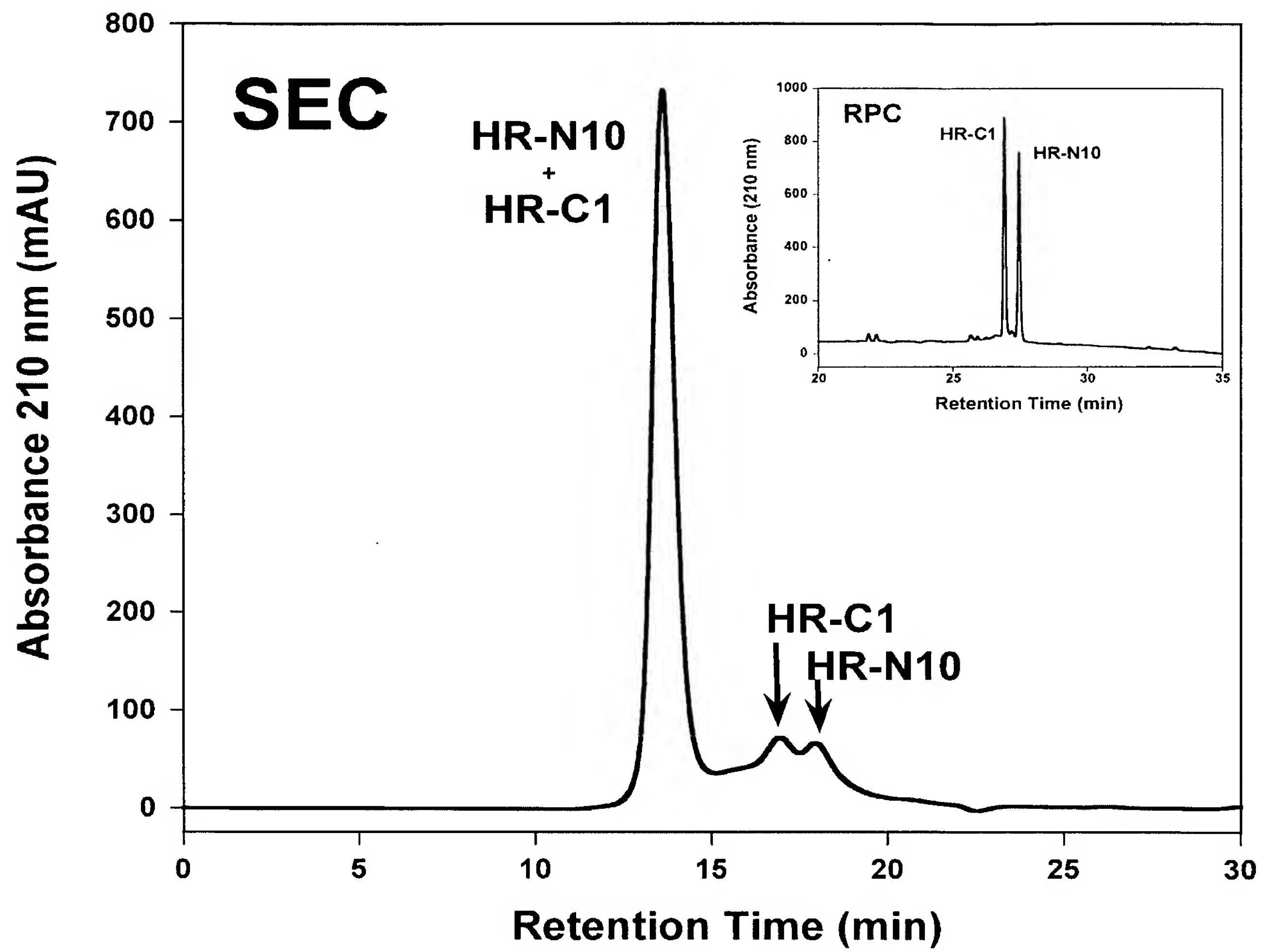


FIG. 6

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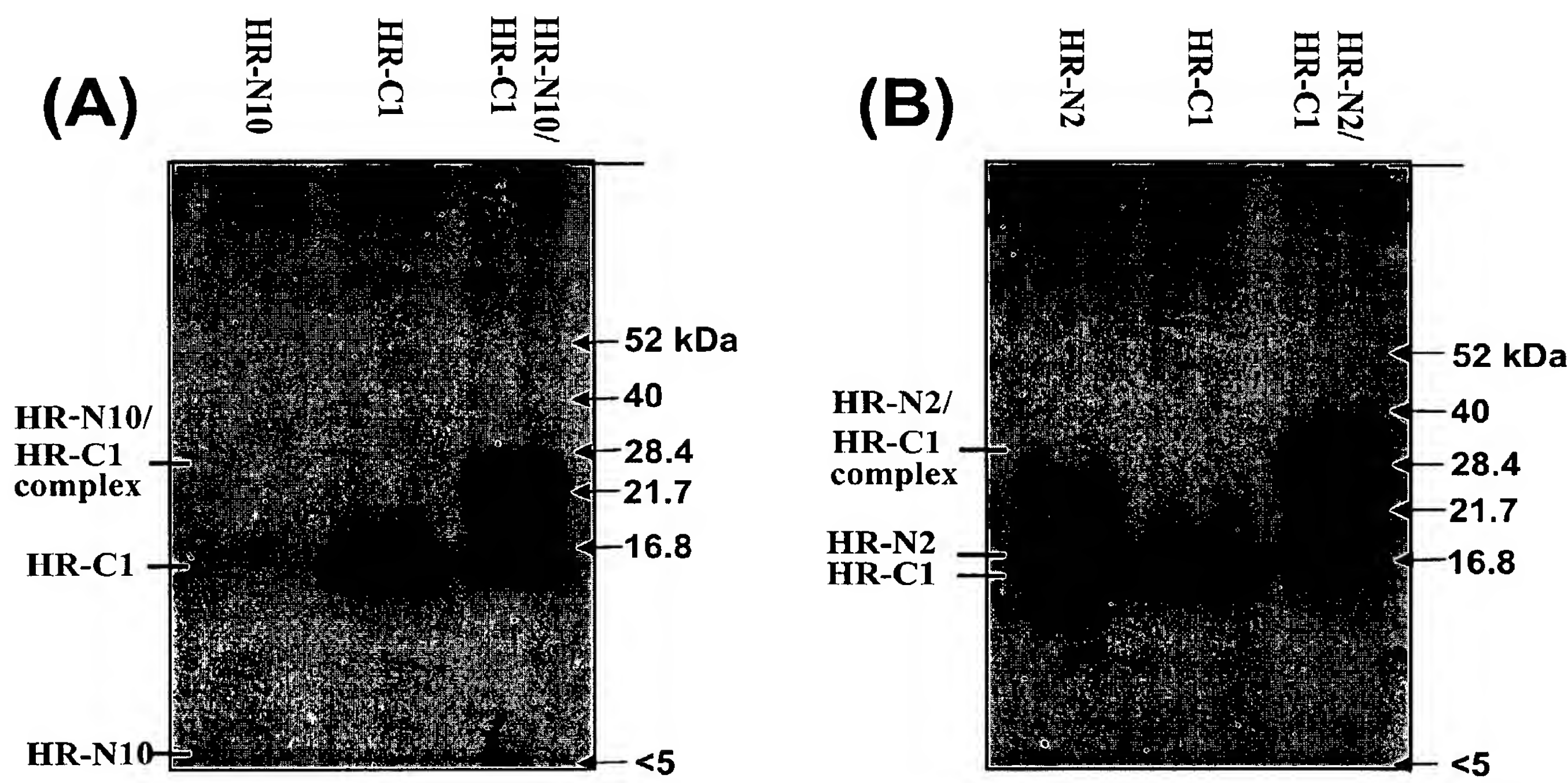


FIG. 7

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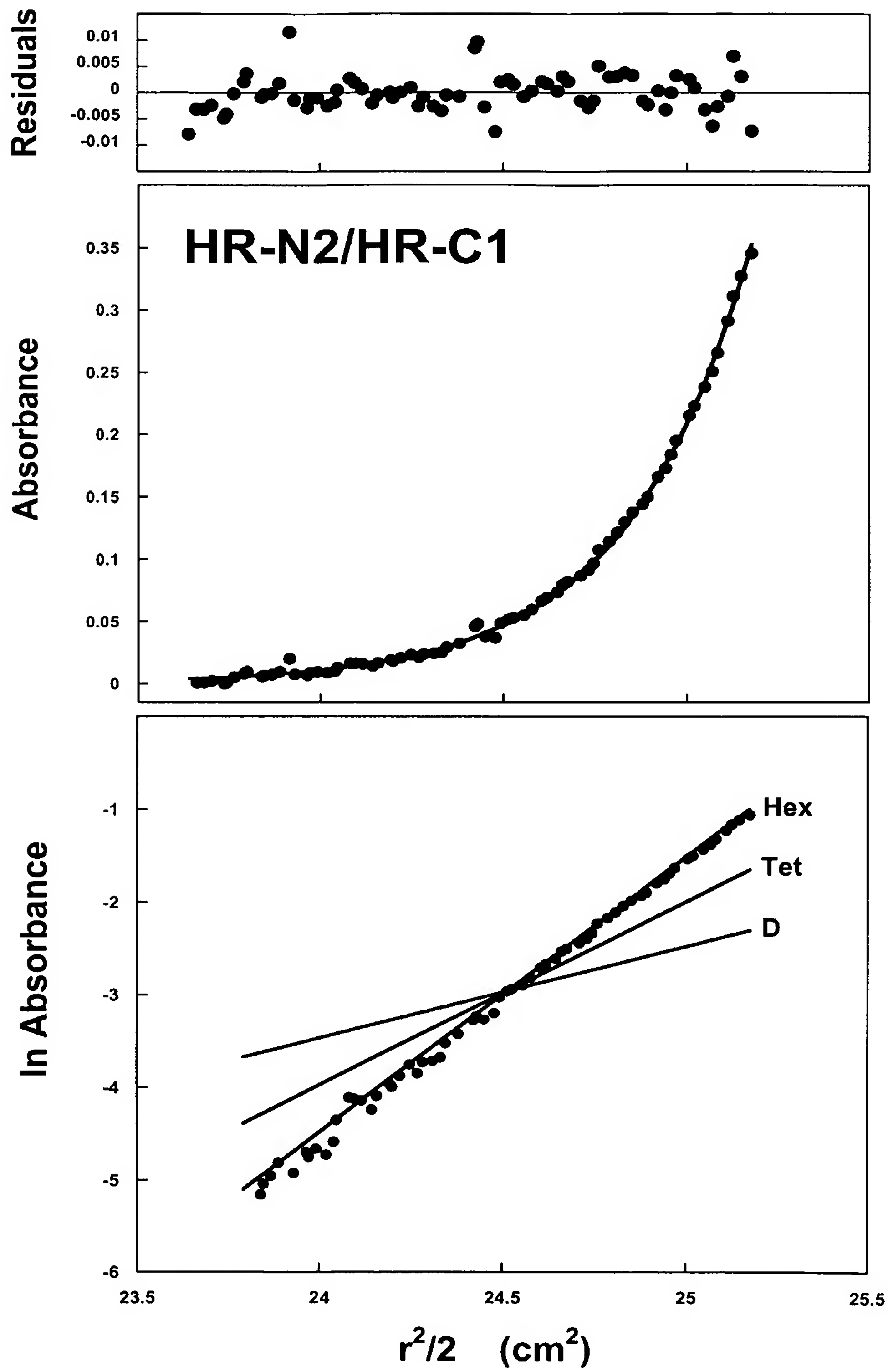


FIG. 8

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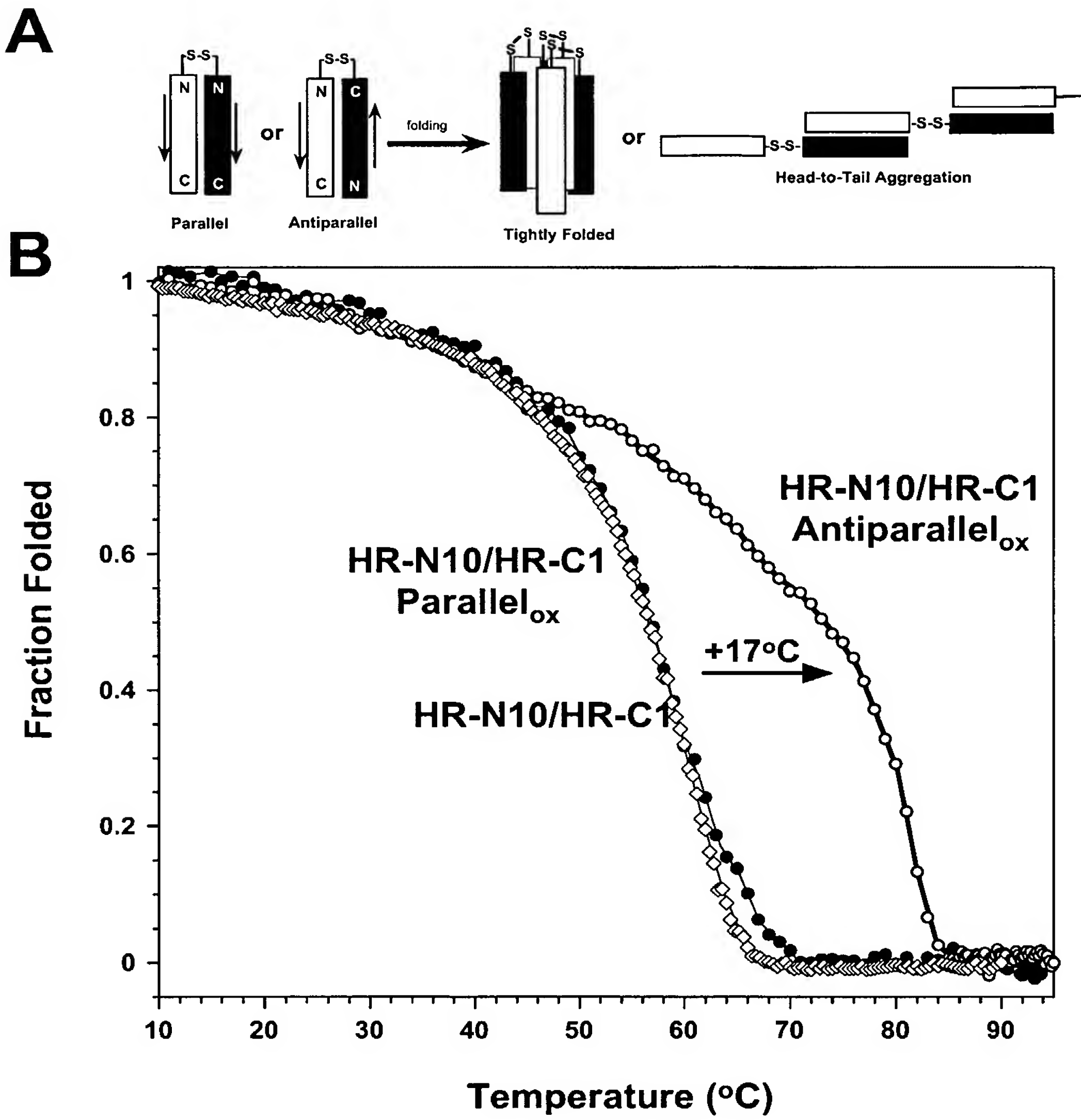


FIG. 9

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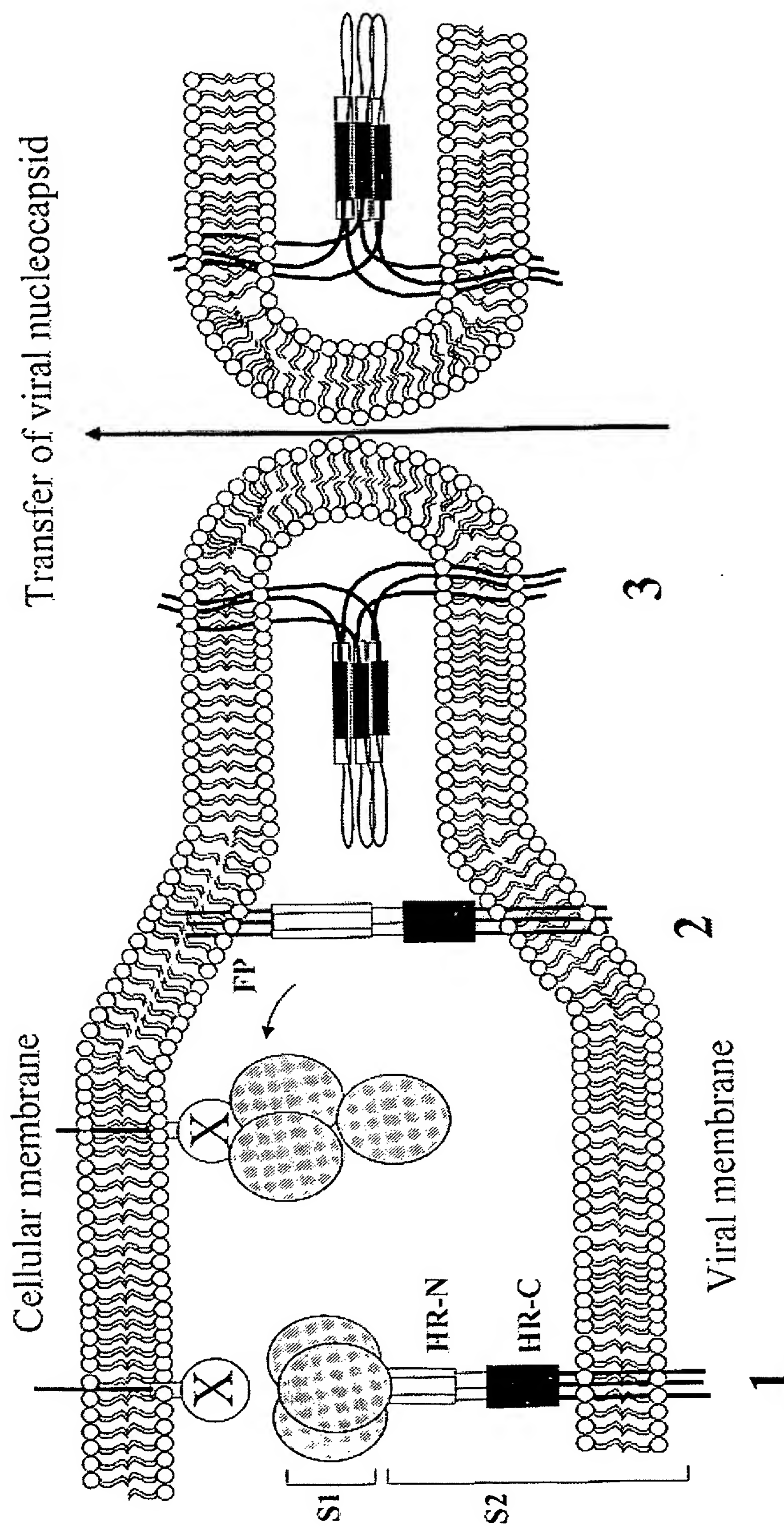


FIG. 10

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HR-N (916-950)

(native)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

(Ala, Lys and Arg substituted)

Ac-IQAALTKTSAALGKLQAAVNRNAAALNKLVKALSS-amide

(Aib=B substituted)

Ac-IQESLTBTSTALGKLQDVVNBNAQALNBLVKQLSS-amide

(Dxg=Z substituted)

Ac-IQESLTZTSTALGKLQDVVNZNAQALNZLVKQLSS-amide

HR-C (1151-1185)

(native)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

(Ala, Lys and Arg substituted)

Ac-IAAINKSVAAIQKEIARLNEVAKALNASLIRLQAL-amide

(Aib=B substituted)

Ac-ISGINBSVVNIQKEIDRLNBVAKNLNBSLIDLQEL-amide

(Dxg=Z substituted)

Ac-ISGINZSVVNIQKEIDRLNZVAKNLNZSLIDLQEL-amide

FIG. 11

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HR-N (916-950)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

1 i,i+4 lactam bridge

Ac-IQESLTTTSTALGKLQEVVNKNAQALNTLVKQLSS-amide


2 i,i+4 lactam bridge

Ac-IQESLTETSTKLGKLQDVVNQNAQALNELVKKLSS-amide


1 i,i+7 bridge

Ac-IQESLTTTSTALGELQDVVNENAQALNTLVKQLSS-amide


HR-C (1151-1185)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

1 i,i+4 lactam bridge

Ac-ISGINASVVNIQKEIERLNKVAKNLNESLIDLQEL-amide


2 i,i+4 lactam bridge

Ac-ISGINESVVKIQKEIDRLNEVAKNLNESLIKLQEL-amide


1 i,i+7 bridge

Ac-ISGINASVVNIQEEIDRLNEVAKNLNESLIDLQEL-amide
 = covalent bond

FIG. 12

HR-N (916-950)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

(Ile and Leu substituted into the hydrophobic core)

Ac-IIESLTTTITALGKLIDVLNQNIQALNTLIKQLSS-amide

HR-C (1151-1185)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

(Ile substituted into the hydrophobic core)

Ac-ISGINASIVNIQKEIDRLNEVIKNLNESLIDLQEL-amide

FIG. 13

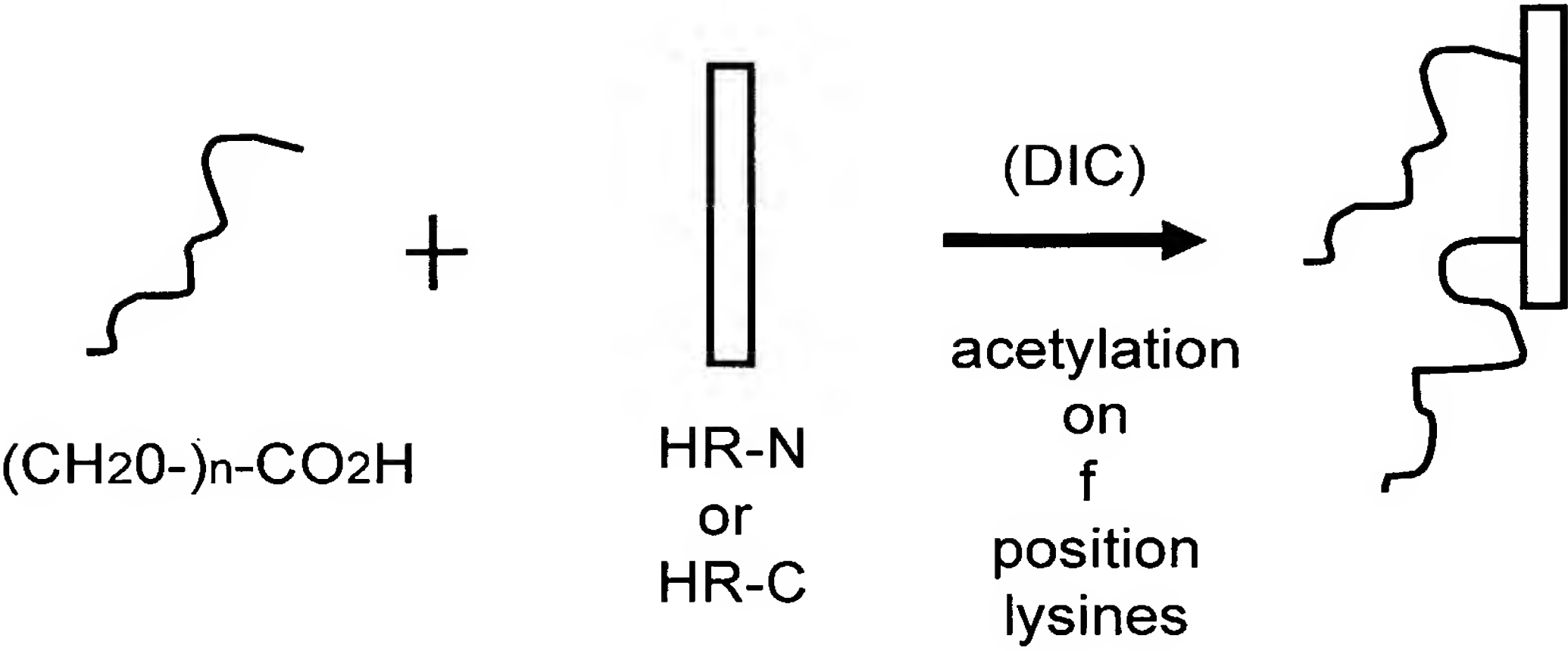


FIG. 14

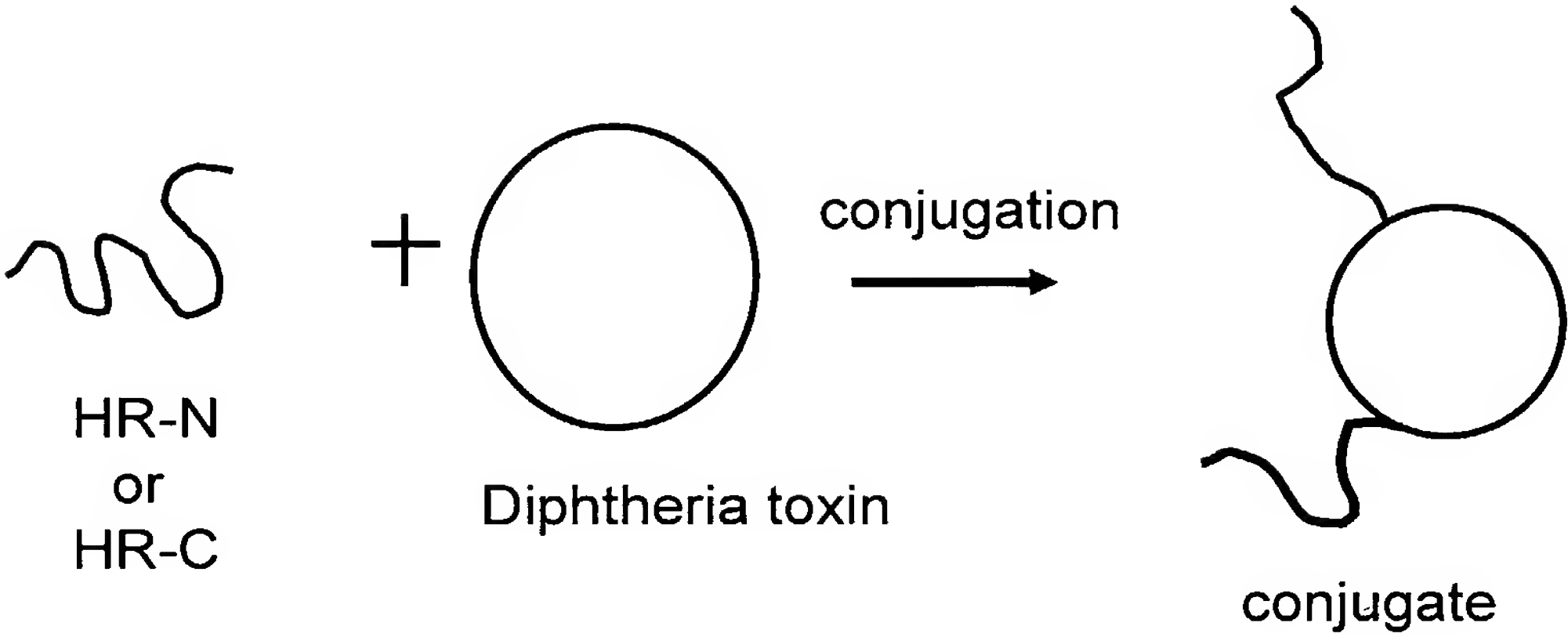


FIG. 15

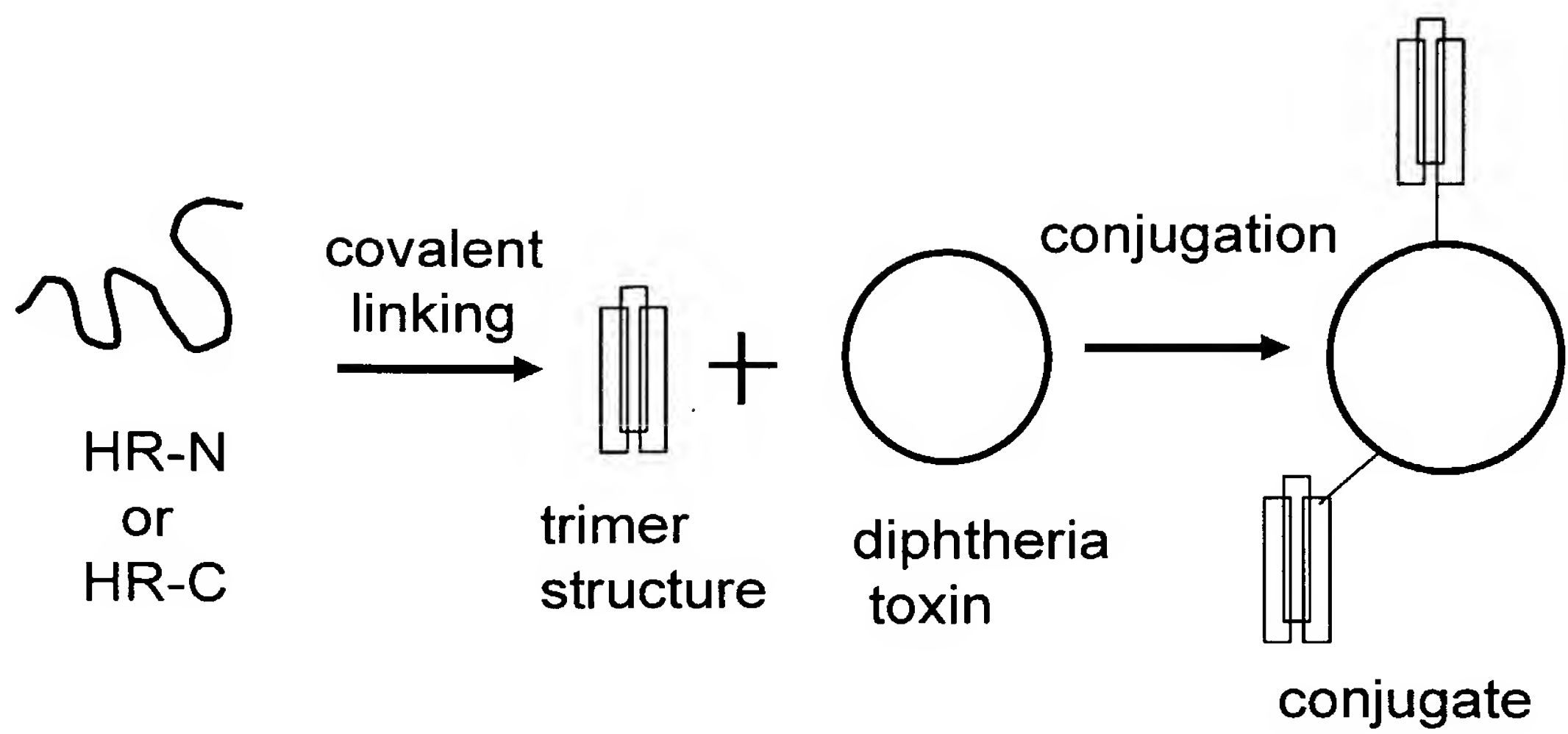


FIG. 16A

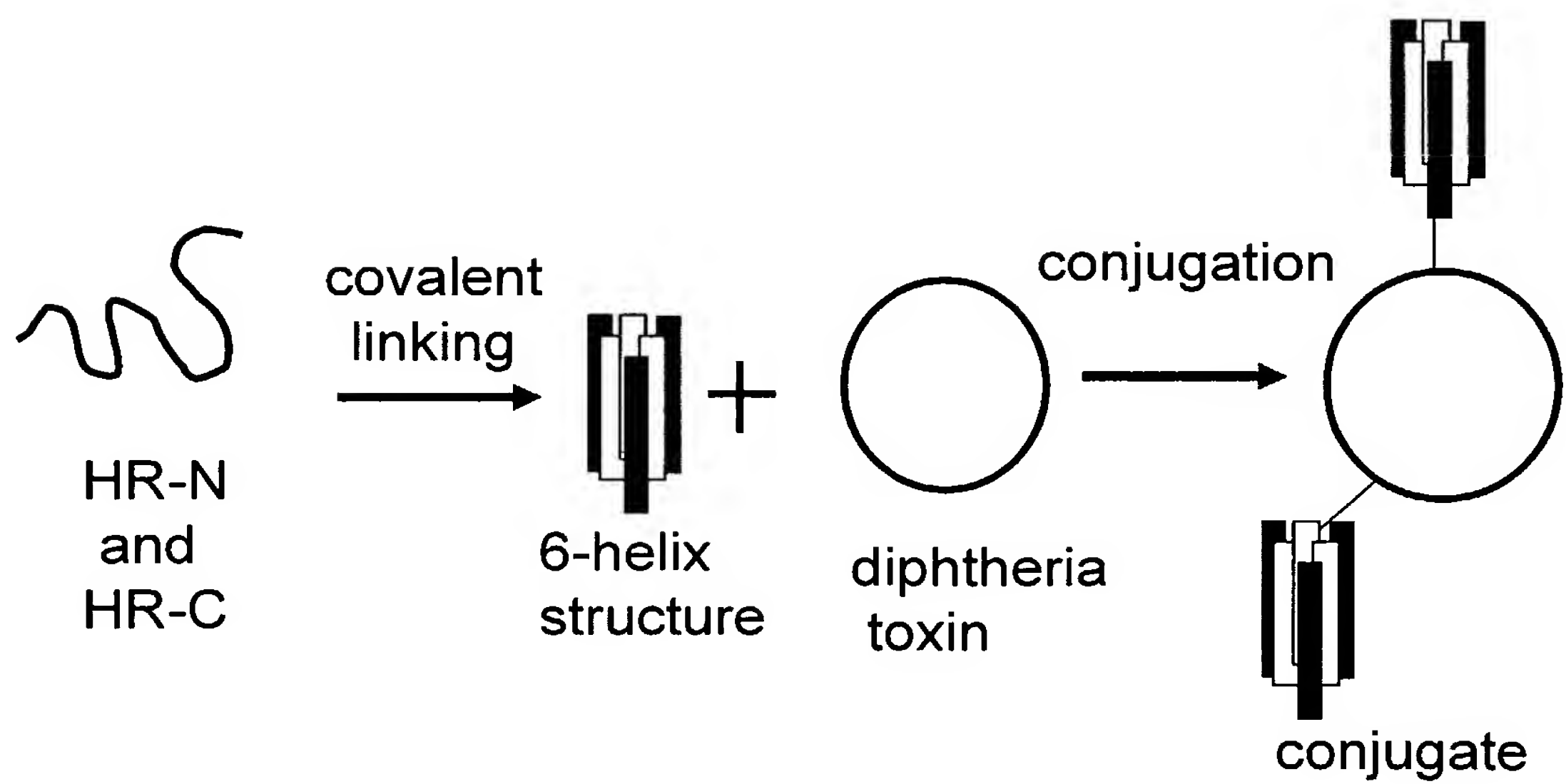


FIG. 16B

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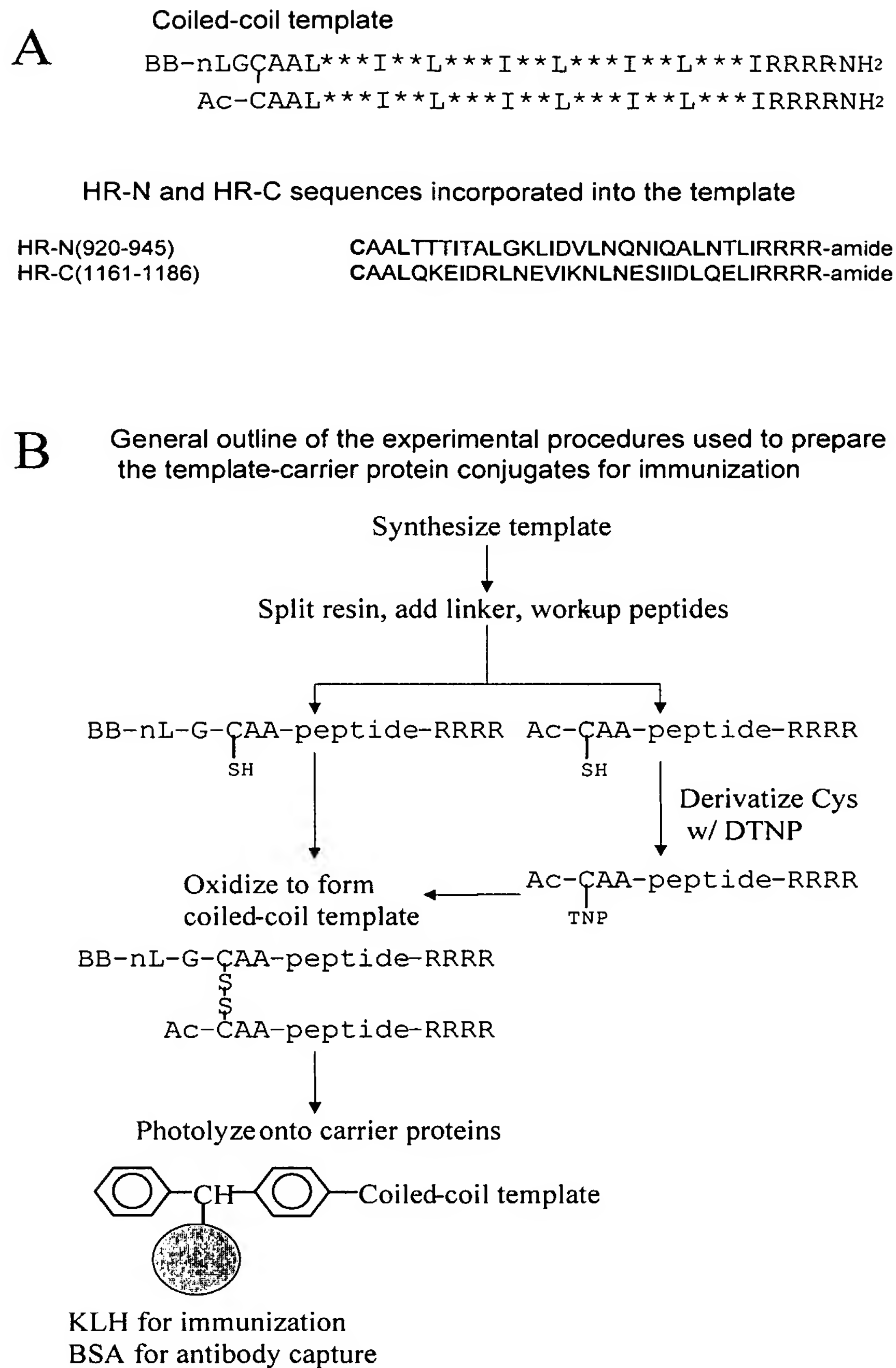


FIG. 17

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HR-N peptides, HR-N1 to HR-N17.

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-N1 (882-973)

ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA
AAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAA
CATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACA
CTTGTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTC
GCGACTTGATAAAGTCGAGGCGGAGGTA

HR-N2 (916-973)

ATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCA
GAATGCTCAAGCATTAAACACACTTGTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAA
GTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTA

HR-N3 (927-973)

TTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACA
ACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTCGCGACTTGATA
AAGTCGAGGCGGAGGTA

HR-N4 (974-1011)

CAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACCT
AATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTAAAATG

HR-N5 (882-916)

ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA
AAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATT

HR-N6 (888-922)

TTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCACAAAACAAATCGCCAACCA
ATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACA

HR-N7 (895-929)

CAAATGTTCTCTATGAGAACCACAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCA
AATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAG

FIG. 18A

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HR-N8 (902-936)

CAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAAC
AACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAG

HR-N9 (909-943)

TTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAA
GCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACA

HR-N10 (916-950)

ATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCA
GAATGCTCAAGCATTAAACACACTTGTTAAACAACCTTAGCTCT

HR-N11 (923-957)

ACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACAC
ACTTGTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGT

HR-N12 (931-965)

CAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACAACCTTAGCTCTAA
TTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTTCGCGA

HR-N13 (938-972)

GCTCAAGCATTAAACACACTTGTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGTGT
GCTAAATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGAG

HR-N14 (945-979)

GTTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTTCGCG
ACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATT

HR-N15 (952-986)

TTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGA
GGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTT

HR-N16 (959-993)

CTAAATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAAT
TACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAA

HR-N17 (966-1000)

CTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCT
TCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATC

FIG. 18B

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HR-C peptides, HR-C1 to HR-C4

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-C1 (1147-1185)

GATGTTGATCTTGGCGACATTTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAAT
TGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTG

HR-C2 (1165-1185)

ATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATT
G

HR-C3 (1158-1185)

GTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATC
ACTCATTGACCTTCAAGAATTG

HR-C4 (1151-1185)

ATTTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGT
CGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTG

Amino acid sequence for SARS peptide HR-C1

HR-C1 (1147-1185)

DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL

FIG. 19

HR-N

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-N (882-1011)

ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAG
AACCAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTAC
AACACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTA
ACACACTTGTTAAACAACCTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATC
CTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATCAGGGCTTCTG
CTAATCTTGCTGCTACTAAAATG

FIG. 20

ATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCACCACTTTTGATG
ATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGGGGGGTTTACTATCCTGATGAAATTTT
TAGATCAGACACTCTTTATTTAACTCAGGATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCAT
ACTATTAATCATAACGTTTGGCAACCCTGTCATACCTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGA
AATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTAT
TAACAATTCTACTAATGTTGTTATACGAGCATGTAACCTTTGAATTGTGTGACAACCCTTTCTTTGCTGTT
TCTAAACCCATGGGTACACAGACACATACTATGATATTCGATAATGCATTTAATTGCACTTTCGAGTACA
TATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAATTTTAAACACTTACGAGAGTTTGTGTT
TAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCT
TCTGGTTTTAACACTTTGAAACCTATTTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCA
TTCTTACAGCCTTTTCACCTGCTCAAGACATTTGGGGCACGTGAGCTGCAGCCTATTTTGTTGGCTATTT
AAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAA
AATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCTA
ATTTACAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACAAACTTGTGTCCTTTTGGAGA
GGTTTTTAATGCTACTAAATTCCTTCTGTCTATGCATGGGAGAGAAAAAAATTTCTAATTGTGTTGCT
GATTACTCTGTGCTCTACAACCTCAACATTTTTTTCAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGT
TGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAAT
AGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGATTTTCATGGGTTGTGTC
CTTGCTTGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATAAATATAGGTATCTTA
GACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCCCTGATGGCAAACCTTG
CACCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGC
TACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACCTTTTAAATGCACCGGCCACGGTTTGTGGACCAA
AATTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTGT
GTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGATTTCACTGAT
TCCGTTTCGAGATCCTAAAACATCTGAAATATTAGACATTTACCTTGCTCTTTTGGGGGTGTAAGTGTA
TTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACTGATGTTTC
TACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTCTACTGGAAACAATGTATTCCAG
ACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAG
CTGGCATTGTGCTAGTTACCATAACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTTA
TACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTT
TCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGTACA
TCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACCTAAATCG
TGCACCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTGAAGTGTTGCTCAAGTCAAACAAATG
TACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTTCACAAATATTACCTGACCCTCTAAAGC
CAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAA
GCAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTT
ACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTG
CCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATAG
GTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCACAAAACAAATCGCCAACCAATTTAAC
AAGGCGATTAGTCAAATTCAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTG
TTAACCAGAATGCTCAAGCATTAACACACTTGTAAACAACCTTAGCTCTAATTTTGGTGCAATTTCAAG
TGTGCTAAATGATATCCTTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACA
GGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATCAGGGCTTCTG
CTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAA
GGGCTACCACCTTATGTCCTTCCCACAAGCAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTG
CCATCCCAGGAGAGGAACCTTCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTG
AAGGTGTTTTTGTGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACCTTCTTTTCTCCACAAATAAT
TACTACAGACAATACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTAT
GATCCTCTGCAACCTGAGCTCGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATAACATCAC
CAGATGTTGATCTTGGCGACATTTCAAGGCATTAACGCTTCTGTGCTCAACATTCAAAAAGAAATTGACCG
CCTCAATGAGGTGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAA
TATATTAAATGGCCTTGGTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAA
TCTTGCTTTGTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAA
GTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAA

FIG. 21

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HR-C Native (SEQ ID NO:48).

1150	1161	1171	1181
DISGINASVVN	IQKEIDRLNE	VAKNLNESLI	DLQEL
ga d a d	a d	a d a	d

HR-C Analogue 1 (SEQ ID NO:67). Modulation of the “a” residue position

1150	1161	1171	1181
DISGINASVVN	IQKEIDRLNE	V <u>I</u> KNLNESLI	DLQEL

HR-C Analogue 2 (SEQ ID NO:68). Change of Helical propensity

1150	1161	1171	1181
DISGINASVVN	IQKEI <u>A</u> RLNE	VAK <u>A</u> NLNESLI	DLQEL

HR-C Analogue 3 (SEQ ID NO:69). Change of Helical propensity and modulation of “a” position

1150	1161	1171	1181
DISGINASVVN	IQKEI <u>A</u> RLNE	V <u>I</u> K <u>A</u> NLNESLI	DLQEL

HR-C Analogue 4 (SEQ ID NO:70). Change of Helical propensity

1150	1161	1171	1181
DI <u>A</u> AINASV <u>A</u> N	IQKEI <u>A</u> RLNE	VAK <u>A</u> NLES <u>L</u> A	<u>A</u> LQ <u>A</u> L

HR-C Analogue 5 (SEQ ID NO:71). Introduction of lactam

1150	1161	1171	1181
DISGINASVVN	IQKEI <u>E</u> RLN <u>K</u>	VAKNLNESLI	DLQEL
	[]		

HR-C Analogue 6 (SEQ ID NO:72). Introduction of salt bridge

1150	1161	1171	1181
DISGINASVVN	IQKEI <u>E</u> RLN <u>K</u>	VAKNLNESLI	DLQEL

HR-C Analogue 7 (SEQ ID NO:73).

1150	1161	1171	1181
DI <u>E</u> EIN <u>K</u> <u>K</u> V <u>E</u> E	I <u>Q</u> <u>K</u> KI <u>E</u> ELN <u>K</u>	<u>K</u> A <u>E</u> ELN <u>K</u> <u>K</u> L <u>E</u>	<u>E</u> LQ <u>K</u> <u>K</u>

HR-C Analogue 8 (SEQ ID NO:74). Introduction of salt bridges

1150	1161	1171	1181
DISGINASV <u>V</u> E	I <u>Q</u> <u>K</u> KI <u>E</u> ELN <u>K</u>	<u>K</u> A <u>E</u> ELN <u>K</u> <u>K</u> L <u>I</u>	DLQEL

FIG. 22